40) 7/11/00

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rag.

start

Go Back to previous page

GenCore version 5.1.9
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OM nucleic - protein search, using frame plus n2p model

Run on: July 11, 2006, 06:34:19; Search time 22 Seconds

(without alignments)

7519.132 Million cell updates/sec

Title: US-10-785-114-6

Perfect score: 2202

Sequence: 1 atgaacaacttgctgtgctg.....taaaaataagctgcttataa 1206

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0

Searched: 2589679 segs, 457216429 residues

Total number of hits satisfying chosen parameters: 5179358

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

. Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=x1h

-Q=/abss/ABSSWEB spool/US10785114/runat 11072006 062819 21385/app query.fasta 1

-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02h

-USER=US10785114 @CGN 1 1 165 @runat 11072006 062819 21385 -NCPU=6 -ICPU=3

-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120

-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: A Geneseq 8:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: genesegp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score			ક્ષ				
1 2201 99.9 401 2 AAR99925 Aar99925 Full leng 2 2201 99.9 401 2 AAW53239 Aaw53239 Human OCI 3 2201 99.9 401 6 ABF70997 Abp70997 Human ost 4 2201 99.9 401 6 ABF70997 Add37427 Human ost 5 2201 99.9 401 8 AD68056 Adq68056 Human ost 6 2201 99.9 401 8 AD68056 Adq68056 Human ost 7 2201 99.9 401 8 AD707096 Ad705742 Tumour ne 8 2195 99.7 401 2 AAW55742 Aay05742 Tumour ne 10 2195 99.7 401 2 AAW55030 Aaw890303 Tumour ne 10 2195 99.7 401 2 AAW55030 Aaw890303 Tumour ne 11 22195 99.7 401 3 AABB8715 Aab1875 Auman TTH 12 2195 99.7 401 4 AAB60570 Aab60570 Human TTN 13 2195 99.7 401 4 AAB60570 Aab60570 Human TTN 14 2195 99.7 401 6 AAG31135 Aab18715 Auman TRA 15 2195 99.7 401 6 AAG31135 Aab18715 16 2195 99.7 401 7 ADF16155 Add61625 Human ost 16 2195 99.7 401 7 ADF16153 Adf16151 Human alb 17 2195 99.7 401 7 ADF16151 Adf16151 Human alb 18 2195 99.7 401 7 ADF16152 Adf16152 Human alb 18 2195 99.7 401 7 ADF16152 Adf16152 Human alb 20 2195 99.7 401 7 ADF16152 Adf16152 Human alb 21 2195 99.7 401 7 ADF16152 Adf16152 Human alb 22 2195 99.7 401 7 ADF16155 Adf16152 Human alb 22 2195 99.7 401 7 ADF16150 Adf16151 Human alb 22 2195 99.7 401 7 ADF16154 Adf16154 Human alb 22 2195 99.7 401 7 ADF16155 Adf16152 Human alb 23 2195 99.7 401 7 ADF16154 Adf16154 Human alb 24 2195 99.7 401 7 ADF16154 Adf16154 Human alb 25 2195 99.7 401 7 ADF16155 Adf16152 Human alb 26 2195 99.7 401 7 ADF16154 Adf16154 Human alb 27 2195 99.7 401 7 ADF16155 Adf16154 Human alb 28 2195 99.7 401 7 ADF16156 Adf16156 Human alb 29 2195 99.7 401 7 ADF16157 Adf16152 Human alb 20 2195 99.7 401 7 ADF16157 Adf16154 Human alb 26 2195 99.7 401 7 ADF16156 Adf16166 Human alb 27 2195 99.7 401 7 ADF16156 Adf16166 Human alb 28 2195 99.7 401 7 ADF16157 Adf16192 Human alb 29 2195 99.7 401 7 ADF16156 Adf16196 Human alb 20 2195 99.7 401 9 AEA55153 Aea55153 Human TRA 29 2195 99.7 401 9 AEA55153 Aea55163 Human TRA 29 2195 99.7 401 9 AEA55153 Aea670297 Human TRA 29 2195 99.7 401 9 AEA55153 Aea670297 Human TRA 29 2195 99.7 401 9 AEA55153 Aea657166 Adf15016 Human ost 20 2195 99.7 401 9 AEA55153 Aea	Result		Query				
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32 2195 99.7 401 9 AED07227 Aed07227 Human tum 33 2195 99.7 401 9 AED07297 Aed07297 Human tum 34 2195 99.7 401 9 AED07408 Aed07408 Human tum 35 2195 99.7 986 7 ADF15016 Adf15016 Human alb 36 2195 99.7 986 7 ADF15030 Adf15030 Human alb 37 2191 99.5 401 2 AAR99931 Aar99931 Mutated O 38 2191 99.5 401 2 AAR99932 Aar99932 Mutated O 39 2188 99.4 399 2 AAR99942 Aar99942 Mutated O 40 2187 99.3 401 2 AAW38345 Aaw38345 Human ost 41 2187 99.3 401 3 AAY43400 Aab66976 Aab66976 Aab66976 Aab66976 Aab66976 Aab66976 Aab7323 Abg71823 Abg71823 Abg71823	30	2195	99.7	401	9	AEA55153	
33 2195 99.7 401 9 AED07297 Aed07297 Human tum 34 2195 99.7 401 9 AED07408 Aed07408 Human tum 35 2195 99.7 986 7 ADF15016 Adf15016 Human alb 36 2195 99.7 986 7 ADF15030 Adf15030 Human alb 37 2191 99.5 401 2 AAR99931 Aar99931 Mutated O 38 2191 99.5 401 2 AAR99932 Aar99932 Mutated O 39 2188 99.4 399 2 AAR99942 Aar99942 Mutated O 40 2187 99.3 401 2 AAW38345 Aaw38345 Human ost 41 2187 99.3 401 3 AAY43400 Aay43400 Osteoprot 42 2187 99.3 401 4 AAB66976 Aab66976 Human OPG 43 2187 99.3 401 5 ABG71823 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost	31	2195	99.7	401	9	AEB19868	Aeb19868 Human ost
34 2195 99.7 401 9 AED07408 Aed07408 Human tum 35 2195 99.7 986 7 ADF15016 Adf15016 Human alb 36 2195 99.7 986 7 ADF15030 Adf15030 Human alb 37 2191 99.5 401 2 AAR99931 Aar99931 Mutated O 38 2191 99.5 401 2 AAR99932 Aar99932 Mutated O 39 2188 99.4 399 2 AAR99942 Aar99942 Mutated O 40 2187 99.3 401 2 AAW38345 Aaw38345 Human ost 41 2187 99.3 401 3 AAY43400 Aab66976 Aab66976 Human OPG 43 2187 99.3 401 5 ABG71823 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost	32	2195	99.7	401	9	AED07227	Aed07227 Human tum
35 2195 99.7 986 7 ADF15016 Adf15016 Human alb 36 2195 99.7 986 7 ADF15030 Adf15030 Human alb 37 2191 99.5 401 2 AAR99931 Aar99931 Mutated O 38 2191 99.5 401 2 AAR99932 Aar99932 Mutated O 39 2188 99.4 399 2 AAR99942 Aar99942 Mutated O 40 2187 99.3 401 2 AAW38345 Aaw38345 Human ost 41 2187 99.3 401 3 AAY43400 Aay43400 Osteoprot 42 2187 99.3 401 4 AAB66976 Aab66976 Human OPG 43 2187 99.3 401 5 ABG71823 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost	33	2195	99.7	401	9	AED07297	Aed07297 Human tum
36 2195 99.7 986 7 ADF15030 Adf15030 Human alb 37 2191 99.5 401 2 AAR99931 Aar99931 Mutated O 38 2191 99.5 401 2 AAR99932 Aar99932 Mutated O 39 2188 99.4 399 2 AAR99942 Aar99942 Mutated O 40 2187 99.3 401 2 AAW38345 Aaw38345 Human ost 41 2187 99.3 401 3 AAY43400 Aab66976 Human OPG 43 2187 99.3 401 4 AAB66976 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost		2195		401	9		Aed07408 Human tum
37 2191 99.5 401 2 AAR99931 Aar99931 Mutated O 38 2191 99.5 401 2 AAR99932 Aar99932 Mutated O 39 2188 99.4 399 2 AAR99942 Aar99942 Mutated O 40 2187 99.3 401 2 AAW38345 Aaw38345 Human ost 41 2187 99.3 401 3 AAY43400 Aay43400 Osteoprot 42 2187 99.3 401 4 AAB66976 Aab66976 Human OPG 43 2187 99.3 401 5 ABG71823 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost				986		ADF15016	Adf15016 Human alb
38 2191 99.5 401 2 AAR99932 Aar99932 Mutated O 39 2188 99.4 399 2 AAR99942 Aar99942 Mutated O 40 2187 99.3 401 2 AAW38345 Aaw38345 Human ost 41 2187 99.3 401 3 AAY43400 Aay43400 Osteoprot 42 2187 99.3 401 4 AAB66976 Aab66976 Human OPG 43 2187 99.3 401 5 ABG71823 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost						ADF15030	
39 2188 99.4 399 2 AAR99942 Aar99942 Mutated O 40 2187 99.3 401 2 AAW38345 Aaw38345 Human ost 41 2187 99.3 401 3 AAY43400 Aay43400 Osteoprot 42 2187 99.3 401 4 AAB66976 Aab66976 Human OPG 43 2187 99.3 401 5 ABG71823 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost	37	2191		401	2	AAR99931	Aar99931 Mutated O
40 2187 99.3 401 2 AAW38345 Aaw38345 Human ost 41 2187 99.3 401 3 AAY43400 Aay43400 Osteoprot 42 2187 99.3 401 4 AAB66976 Aab66976 Human OPG 43 2187 99.3 401 5 ABG71823 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost							
41 2187 99.3 401 3 AAY43400 Aay43400 Osteoprot 42 2187 99.3 401 4 AAB66976 Aab66976 Human OPG 43 2187 99.3 401 5 ABG71823 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost							
42 2187 99.3 401 4 AAB66976 Aab66976 Human OPG 43 2187 99.3 401 5 ABG71823 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost							
43 2187 99.3 401 5 ABG71823 Abg71823 Wild type 44 2187 99.3 401 6 ABP55109 Abp55109 Human ost							
44 2187 99.3 401 6 ABP55109 Abp55109 Human ost							
					_		
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	45	2187	99.3	401	6	AAE34363	Aae34363 Human ost

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rai.

start

Go Back to previous page

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GenCore version 5.1.9
                 Copyright (c) 1993 - 2006 Biocceleration Ltd.
OM nucleic - protein search, using frame_plus_n2p model
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Perfect score: 2202
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               Ygapop 10.0, Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop
                       6.0 , Delext
                                      7.0
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Total number of hits satisfying chosen parameters: 1301182
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Maximum DB seq length: 2000000000
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                Maximum Match 100%
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http://es/ScoreAccessWeb/GetItem.action?AppId=10785114&seqId=559655&ItemName=... 7/14/2006

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

			용				
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	2	2201	99.9	401	2	US-09-338-063A-5	Sequence 5, Appli
	3	2195	99.7	401	2	US-09-153-927-1	Sequence 1, Appli
	4	2195	99.7	401	2	US-09-072-993C-1	Sequence 1, Appli
	5	2191	99.5	401	2	US-10-232-858-62	Sequence 62, Appl
	6	2191	99.5	401	2	US-10-232-858-63	Sequence 63, Appl
	7	2191	99.5	401	2	US-10-232-858-64	Sequence 64, Appl
	8	2191	99.5	401	2	US-10-232-858-65	Sequence 65, Appl
	9	2191	99.5	401	2	US-10-232-858-66	Sequence 66, Appl
	10	2191	99.5	401	2	US-09-338-063A-62	Sequence 62, Appl
	11	2191	99.5	401	2	US-09-338-063A-63	Sequence 63, Appl
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	15	2188	99.4	399	2	US-10-232-858-73	Sequence 73, Appl
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	17	2187	99.3	401	2	US-08-974-022-6	Sequence 6, Appli
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	19	2187	99.3	401	2	US-08-795-445A-6	Sequence 6, Appli
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	22	2187	99.3	401	2	US-08-795~446B-6	Sequence 6, Appli
	23	2187	99.3	401	2	US-08-706-945D-128	Sequence 128, App
	24	2187	99.3	401	2	US-08-577-788C-6	Sequence 6, Appli
	25	2187	99.3	401	2	ÚS-08-577-788C-56	Sequence 56, Appl
	26	2187	99.3	401	2	US-09-064-832-2	Sequence 2, Appli
	27	2183	99.1	401	3	US-09-613-591F-125	Sequence 125, App
	28	2155	97.9	393	2	US-10-232-858-79	Sequence 79, Appl
	29	2155	97.9	393	2	US-09-338-063A-79	Sequence 79, Appl
	30	2152.5	97.8	394	2	US-10-232-858-9	Sequence 9, Appli
	31	2152.5	97.8	394	2	US-09-338-063A-9	Sequence 9, Appli
	32	2146	97.5	391	2	US-10-232-858-106	Sequence 106, App
	33	2146	97.5	391	2	US-09-338-063A-106	Sequence 106, App
	34	2087	94.8	380	2	US-10-232-858-4	Sequence 4, Appli
	35	2087	94.8	380	2	US-09-338-063A-4	Sequence 4, Appli
	36	2070	94.0	380	3	US-09-613-591F-139	Sequence 139, App
	37	1976	89.7	364	2	US-08-706-945D-142	Sequence 142, App
	38	1972.5	89.6	362	2	US-10-232-858-11	Sequence 11, Appl
	39	1972.5	89.6	362	2	US-09-338-063A-11	Sequence 11, Appl
	40	1956	88.8	363	2	US-10-232-858-69	Sequence 69, Appl
	41	1956	88.8	363	2	US-09-338-063A-69	Sequence 69, Appl
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	43	1944	88.3	351	2	US-09-338-063A-74	Sequence 74, Appl
	44	1933	87.8	359	2	US-10-232-858-70	Sequence 70, Appl
	45	1933	87.8	359	2	US-09-338-063A-70	Sequence 70, Appl
			· -		-		

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rapbm.

GenCore version 5.1.9

start

Go Back to previous page

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Perfect score: 2202
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Scoring table: BLOSUM62
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                                      7.0
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      Pred. No. is the number of results predicted by chance to have a
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     and is derived by analysis of the total score distribution.
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. 23	2195	99.7	401	5	US-10-966-845-2	Sequence 2, Appli
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25	2195	99.7	401	5	US-10-775-204-529	Sequence 529, App
26	2195	99.7	401	5	US-10-775-204-542	Sequence 542, App
27	2195		401	5	US-10-775-204-1238	Sequence 1238, Ap
28	2195	99.7	401	5	US-10-775-204-1239	Sequence 1239, Ap
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44	2195	99.7	401	5	US-10-931-196-52 US-10-942-042-52	Sequence 52, Appl
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4.5	2133	22.1	200	5	03-10-113-204-312	Sequence 312, App

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rapbn.

start

Go Back to previous page

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GenCore version 5.1.9
                 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                Fgapop 6.0 , Fgapext 7.0
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Command line parameters:
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Database :
                Published Applications AA New:*
               1: /EMC Celerra SIDS3/ptodata/1/pubpaa/US09 NEW PUB.pep:*
               2: /EMC Celerra SIDS3/ptodata/1/pubpaa/US06 NEW PUB.pep:*
               3: /EMC_Celerra SIDS3/ptodata/1/pubpaa/US07 NEW PUB.pep:*
               4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08 NEW PUB.pep:*
               5: /EMC Celerra SIDS3/ptodata/1/pubpaa/PCT NEW PUB.pep:*
                6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                7: /EMC Celerra SIDS3/ptodata/1/pubpaa/US11 NEW PUB.pep:*
                8: /EMC Celerra SIDS3/ptodata/1/pubpaa/US60 NEW PUB.pep:*
      Pred. No. is the number of results predicted by chance to have a
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		8				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	2195	99.7	401	 7	US-11-175-714-54	Sequence 54, Appl
2	1726.5	78.4	349	7	US-11-175-714-67	Sequence 67, Appl
3	347	15.8	258	6	US-10-643-589-4	Sequence 4, Appli
4	340	15.4	355	6	US-10-504-973-33	Sequence 33, Appl
5	330	15.0	461	6	US-10-511-937-2945	Sequence 2945, Appl
6	330	15.0	461	7	US-11-183-218-32	Sequence 32, Appl
7	301.5	13.7	655	6	US-10-505-928-843	Sequence 843, App
8	301.5	13.7	655	6	US-10-196-749-418	Sequence 418, App
9	287.5	13.1	289	7	US-11-170-797-12	
10	267.3	12.1	278	7		Sequence 12, Appl
11	264	12.1	197	7	US-11-170-797-16 US-11-211-917-139	Sequence 16, Appl
12	264			6		Sequence 139, App
		12.0	277		US-10-511-937-2518	Sequence 2518, Ap
13	264	12.0	277	7	US-11-170-797-5	Sequence 5, Appli
14	257.5	11.7	237	6	US-10-504-973-22	Sequence 22, Appl
15	252.5	11.5		7	US-11-170-797-19	Sequence 19, Appl
16	198	9.0	153	7	US-11-211-917-140	Sequence 140, App
17	188.5	8.6	250	7	US-11-320-192-7	Sequence 7, Appli
18	188	8.5	256	6	US-10-623-808-6	Sequence 6, Appli
19	188	8.5	256	7	US-11-128-422-6	Sequence 6, Appli
20	187.5	8.5	243	7	US-11-320-192-9	Sequence 9, Appli
21	187.5	8.5	243	7	US-11-320-192-12	Sequence 12, Appl
22	187.5	8.5	251	7	US-11-320-192-8	Sequence 8, Appli
23	186.5	8.5	250	7	US-11-320-192-11	Sequence 11, Appl
24	184.5	8.4	250	7	US-11-320-192-10	Sequence 10, Appl
25	177	8.0	255	6	US-10-623-808-8	Sequence 8, Appli
26	177	8.0	255	6	US-10-539-257-2	· Sequence 2, Appli
27	177	8.0	255	7	US-11-128-422-8	Sequence 8, Appli
28	174	7.9	277	6	US-10-511-937-2455	Sequence 2455, Ap
29	168	7.6	247	6	US-10-504-973-6	Sequence 6, Appli
30.		7.0	440	7	US-11-254-182-49	Sequence 49, Appl
31	144.5	6.6	468	6	US-10-511-937-2595	Sequence 2595, Ap
32	143	6.5	241	7	US-11-351-617-4	Sequence 4, Appli
33	143	6.5	241	7	US-11-315-825-3	Sequence 3, Appli
34	142.5	6.5	411	7	US-11-254-182-47	Sequence 47, Appl
35	142.5	6.5	411	7	US-11-297-319-1	Sequence 1, Appli
36	138	6.3	228	7	US-11-351-617-6	Sequence 6, Appli
37	138	6.3	311	7	US-11-351-617-8	Sequence 8, Appli
38	125	5.7	417	6	US-10-505-928-793	Sequence 793, App
39	123	5.6	228	7	US-11-351-617-2	Sequence 2, Appli
40	123	5.6	228	7	US-11-315-825-24	Sequence 24, Appl
41	121.5	5.5	969	6	US-10-505-928-94	Sequence 94, Appl
42	119	5.4	111	7	US-11-211-917-141	Sequence 141, App
43	116	5.3	1418	7	US-11-217-997-38	Sequence 38, Appl
44	114.5	5.2	408	7	US-11-175-714-140	Sequence 140, App
45	114.5	5.2	430	7	US-11-175-714-138	Sequence 138, App

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rpr.

start

Go Back to previous page

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GenCore version 5.1.9
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OM nucleic - protein search, using frame plus n2p model

Run on: July 11, 2006, 06:38:44; Search time 5.8 Seconds

(without alignments)

6001.935 Million cell updates/sec

Title: US-10-785-114-6

Perfect score: 2202

Sequence: 1 atgaacaacttgctgtgctg.....taaaaataagctgcttataa 1206

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

- -MODEL=frame+ n2p.model -DEV=x1h
- -Q=/abss/ABSSWEB spool/US10785114/runat 11072006 062823 21423/app query.fasta 1
- -DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
- -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
- -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
- -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02h
- -USER=US10785114 @CGN 1 1 32 @runat 11072006 062823 21423 -NCPU=6 -ICPU=3
- -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
- -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
- -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: PIR 80:*

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	344	15.6	474	2	B38634	tumor necrosis fac
2	343	15.6	459	2	I48854	gene murine tumour
3	330	15.0	461	1	A35356	tumor necrosis fac
4	329	14.9	651	2	JC7705	death receptor-6 -
5	287.5	13.1	305	2	A46476	B cell-associated
6	264	12.0	277	2	A60771	B-cell activation
7	239.5	10.9	435	2	154182	tumor necrosis fac
8	237	10.8	348	2	T28623	hypothetical prote
9	231.5	10.5	349	2	D36858	gene G4R protein -
10	228.5	10.4	349	2	D72175	G2R protein - vari
11	225	10.2	325	2	B43692	T2 protein - rabbi
12	219	9.9	326	1	GQVZML	T2 protein - myxom
13	189.5	8.6	425	1	A26431	nerve growth facto
14	188.5	8.6	427	1	GQHUN	nerve growth facto
15	188	8.5	256	2	B32393	T-cell antigen 4-1
16	187	8.5	461	1	GQRTT1	tumor necrosis fac
17	185.5	8.4	314	2	137383	FAS soluble protei
18	183	8.3	335	2	A40036	· apoptosis-mediatin
19	177.5	8.1	416	1	JN0006	nerve growth facto
20	177	8.0	255	2	I38426	lymphocyte activat
21	176	8.0	454	1	GQMST1	tumor necrosis fac
22	174	7.9	277	2	137552	OX40 homolog - hum
23	173.5	7.9	455	1	GQHUT1	tumor necrosis fac
24	172	7.8	271	2	S12783	OX40 antigen precu
25	168	7.6	461	2	JC4302	tumor necrosis fac
26	158	7.2	595	2	A42086	CD30 antigen precu
27	152.5	6.9	272	2	148700	gene ox40 protein
28	152	6.9	324	2	JC2395	Fas antigen precur
29	145	6.6	643	2	T25473	hypothetical prote
30	144	6.5	327	2	A46484	apoptosis-mediatin
31	142.5	6.5	1548	2	\$34583	serine proteinase
32	137.5	6.2	2823	2	F87908	protein T22A3.8 [i
33	137.5	6.2	2823	2	T23064	hypothetical prote
34	137.5	6.2	3102	2	T43291	laminin alpha chai
35	133	6.0	1252	2	S36016	oocyst wall protei
36	130	5.9	398	2	T33383	hypothetical prote
37	129.5	5.9	1369	2	\$70713	protein-tyrosine k
38	129.5	5.9	1786	1	MMHUB1	laminin beta-1 cha
39	129.5	5.9	2610	2	T20968	hypothetical prote
40	129.5	5.9	2918	2	A54105	fibrillin-2 precur
41	129	5.9	1790	1	MMFFB1	laminin beta-1 cha
42	128.5	5.8	899	2	G02428	subtilisin-like pr
43	128.5	5.8	915	2	JC6148	subtilisin-like pr
44	128	5.8	3712	2	\$18253	laminin alpha-1 ch
45	125.5	5.7	1786	1	MMMSB1	laminin beta-1 cha

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-

<u>start</u>

Go Back to previous page

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OM nucleic - protein search, using frame_plus_n2p model

July 11, 2006, 06:35:56; Search time 44.9 Seconds Run on:

(without alignments)

7453.689 Million cell updates/sec

Title: US-10-785-114-6

Perfect score: 2202

Sequence: 1 atgaacaacttgctgtgctg.....taaaaataagctgcttataa 1206

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext

2849598 seqs, 925015592 residues Searched:

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp

-Q=/abss/ABSSWEB spool/US10785114/runat 11072006 062820 21400/app query.fasta 1

-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss05p

-USER=US10785114_@CGN_1_1_381_@runat_11072006_062820_21400 -NCPU=6 -ICPU=3

-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120

-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 7.2:*

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1: uniprot sprot:* 2: uniprot trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Result

> Score Match Length DB ID No.

Description

1	2201	99.9	401	2	Q53FX6_HUMAN	Q53fx6	homo sapien
2	2195	99.7	401	1	TR11B_HUMAN	000300	homo sapien
3	1909	86.7	401	1	TR11B_RAT		rattus norv
4	1909	86.7	401	2	Q6PI12 MOUSE	Q6pi12	mus musculu
5	1895	86.1	401	1	TR11B MOUSE	008712	mus musculu
6	1895	86.1	401	2	Q3UK97 MOUSE	Q3uk97	m 11 days p
7	1596.5	72.5	402	2	Q4F9K2_CHICK	Q4f9k2	gallus gall
8	1038.5	47.2	387	2	Q6GLN3_XENLA	Q6gln3	xenopus lae
9	608	27.6	146	2	Q7ZZY4_CHICK	Q7zzy4	gallus gall
10	584.5	26.5	480	2	Q4SH87_TETNG	Q4sh87	tetraodon n
11	450	20.4	186	2	Q7ZZY5_CHICK		gallus gall
12	445	20.2	300	1	TNR6B_HUMAN		homo sapien
13	408.5	18.6	302	2			salvelinus
14	380.5	17.3	285	2	Q90W71_ONCMY		oncorhynchu
15	372.5	16.9	285	2	_		oncorhynchu
16	364	16.5	286	2	Q6NW61_BRARE	Q6nw61	brachydanio
17	354	16.1	561	2	Q4SH86_TETNG	Q4sh86	tetraodon n
18	347	15.8	474	2	Q3U2A9_MOUSE	Q3u2a9	mus musculu
19	344	15.6	474	1	TNR1B_MOUSE		mus musculu
20	344	15.6	474	2	Q545P4_MOUSE		m adult mal
21	344	15.6	637	2	Q5TYN2_BRARE		brachydanio
22	343	15.6	459	2	Q62327_MOUSE		mus musculu
23	333	15.1	461	2			rattus norv
24	333	15.1	474	1	TNR1B_RAT		rattus norv
25	333	15.1	474	2	Q5YLP0_RAT		rattus norv
26	330	15.0	461	1	TNR1B_HUMAN		h tumor nec
27	330	15.0	461	2	Q5THJ6_HUMAN		homo sapien
28	329	14.9	651	2	Q98SM6_CHICK		gallus gall
29	322.5	14.6	433	2	Q91ZM6_RAT		rattus norv
30	301.5	13.7	655	1	TNR21_HUMAN		homo sapien
31	298	13.5	483	2			paralichthy
32	297	13.5	457	2	Q8IVS6_HUMAN		homo sapien
33	295	13.4	655	2	Q3UYG3_MOUSE		mus musculu
34	294	13.4	267	2	Q3UPV2_MOUSE		mus musculu
35	294	13.4	459	2	Q3MHI9_BOVIN		bos taurus
36	294	13.4	655	1	TNR21_MOUSE		mus musculu
37	294	13.4	655	2	Q543Y9_MOUSE		mus musculu
38	293	13.3	289	2	Q3U7C9_MOUSE		mus musculu
39	292.5	13.3	289	2	Q4QQW2_RAT		rattus norv
40 -		13.2	289	2	Q3U799_MOUSE		mus musculu
41	290.5	13.2	289	2	Q3TSL2_MOUSE		m 10 days n
42	290.5	13.2	289	2	Q3UBH3_MOUSE		mus musculu
43	290.5	13.2	289	2	Q8K2X6_MOUSE		mus musculu
44	287.5	13.1	289	1	_		mus musculu
45	287.5	13.1	289	2	Q542B1_MOUSE	Q542b1	m activated